

Rec'd PCT/PTO 13 OCT 2004



10/510121 PCT

## RAW SEQUENCE LISTING

DATE: 10/13/2004

PATENT APPLICATION: US/10/510,121

TIME: 14:59:06

Input Set : A:\SEQUENCE LISTING (231060.ST25).txt

Output Set: N:\CRF4\10132004\J510121.raw

3 <110> APPLICANT: SUGARU, Eiji  
 4 ICHIHARA, Junji  
 5 taiji, Matsuo  
 8 <120> TITLE OF INVENTION: Novel Blood Sugar Controller and Method of Screening the  
 Same  
 10 <130> FILE REFERENCE: 231060  
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/510,121  
 C--> 12 <141> CURRENT FILING DATE: 2004-10-04  
 12 <150> PRIOR APPLICATION NUMBER: JP 2002-101781  
 13 <151> PRIOR FILING DATE: 2002-04-03  
 15 <150> PRIOR APPLICATION NUMBER: PCT/JP03/04260  
 16 <151> PRIOR FILING DATE: 2003-04-03  
 18 <160> NUMBER OF SEQ ID NOS: 10  
 20 <170> SOFTWARE: PatentIn version 3.1  
 22 <210> SEQ ID NO: 1  
 23 <211> LENGTH: 1104  
 24 <212> TYPE: DNA  
 25 <213> ORGANISM: Homo sapiens  
 27 <220> FEATURE:  
 28 <221> NAME/KEY: CDS  
 29 <222> LOCATION: (1)..(1104)  
 30 <223> OTHER INFORMATION:  
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 34 Met Val Leu Glu Val Ser Asp His Gln Val Leu Asn Asp Ala Glu Val  
 35 1 5 10 15  
 36 gcc gcc ctc ctg gag aac ttc agc tct tcc tat gac tat gga gaa aac 96  
 37 Ala Ala Leu Leu Glu Asn Phe Ser Ser Ser Tyr Asp Tyr Gly Glu Asn  
 38 20 25 30  
 39 gag agt gac tcg tgc tgt acc tcc ccg ccc tgc cca cag gac ttc agc 144  
 40 Glu Ser Asp Ser Cys Cys Thr Ser Pro Pro Cys Pro Gln Asp Phe Ser  
 41 35 40 45  
 42 ctg aac ttc gac cgg gcc ttc ctg cca gcc ctc tac agc ctc ctc ttt 192  
 43 Leu Asn Phe Asp Arg Ala Phe Leu Pro Ala Leu Tyr Ser Leu Leu Phe  
 44 50 55 60  
 45 ctg ctg ggg ctg ctg ggc aac ggc gcg gtg gca gcc gtg ctg ctg agc 240  
 46 Leu Leu Gly Leu Leu Gly Asn Gly Ala Val Ala Ala Val Leu Leu Ser  
 47 65 70 75 80  
 48 cgg cgg aca gcc ctg agc agc acc gac acc ttc ctg ctc cac cta gct 288  
 49 Arg Arg Thr Ala Leu Ser Ser Thr Asp Thr Phe Leu Leu His Leu Ala  
 50 85 90 95  
 51 gta gca gac acg ctg ctg gtg ctg aca ctg ccg ctc tgg gca gtg gac 336  
 52 Val Ala Asp Thr Leu Leu Val Leu Thr Leu Pro Leu Trp Ala Val Asp  
 53 100 105 110



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54 gct gcc gtc cag tgg gtc ttt ggc tct ggc ctc tgc aaa gtg gca ggt      384
55 Ala Ala Val Gln Trp Val Phe Gly Ser Gly Leu Cys Lys Val Ala Gly
56      115      120      125
57 gcc ctc ttc aac atc aac ttc tac gca gga gcc ctc ctg ctg gcc tgc      432
58 Ala Leu Phe Asn Ile Asn Phe Tyr Ala Gly Ala Leu Leu Leu Ala Cys
59      130      135      140
60 atc agc ttt gac cgc tac ctg aac ata gtt cat gcc acc cag ctc tac      480
61 Ile Ser Phe Asp Arg Tyr Leu Asn Ile Val His Ala Thr Gln Leu Tyr
62 145      150      155      160
63 cgc cgg ggg ccc ccg gcc cgc gtg acc ctc acc tgc ctg gct gtc tgg      528
64 Arg Arg Gly Pro Pro Ala Arg Val Thr Leu Thr Cys Leu Ala Val Trp
65      165      170      175
66 ggg ctc tgc ctg ctt ttc gcc ctc cca gac ttc atc ttc ctg tcg gcc      576
67 Gly Leu Cys Leu Leu Phe Ala Leu Pro Asp Phe Ile Phe Leu Ser Ala
68      180      185      190
69 cac cac gac gag cgc ctc aac gcc acc cac tgc caa tac aac ttc cca      624
70 His His Asp Glu Arg Leu Asn Ala Thr His Cys Gln Tyr Asn Phe Pro
71      195      200      205
72 cag gtg ggc cgc acg gct ctg cgg gtg ctg cag ctg gtg gct ggc ttt      672
73 Gln Val Gly Arg Thr Ala Leu Arg Val Leu Gln Leu Val Ala Gly Phe
74      210      215      220
75 ctg ctg ccc ctg ctg gtc atg gcc tac tgc tat gcc cac atc ctg gcc      720
76 Leu Leu Pro Leu Leu Val Met Ala Tyr Cys Tyr Ala His Ile Leu Ala
77 225      230      235      240
78 gtg ctg ctg gtt tcc agg ggc cag cgg cgc ctg cgg gcc atg cgg ctg      768
79 Val Leu Leu Val Ser Arg Gly Gln Arg Arg Leu Arg Ala Met Arg Leu
80      245      250      255
81 gtg gtg gtg gtc gtg gtg gcc ttt gcc ctc tgc tgg acc ccc tat cac      816
82 Val Val Val Val Val Val Ala Phe Ala Leu Cys Trp Thr Pro Tyr His
83      260      265      270
84 ctg gtg gtg ctg gtg gac atc ctc atg gac ctg ggc gct ttg gcc cgc      864
85 Leu Val Val Leu Val Asp Ile Leu Met Asp Leu Gly Ala Leu Ala Arg
86      275      280      285
87 aac tgt ggc cga gaa agc agg gta gac gtg gcc aag tcg gtc acc tca      912
88 Asn Cys Gly Arg Glu Ser Arg Val Asp Val Ala Lys Ser Val Thr Ser
89      290      295      300
90 ggc ctg ggc tac atg cac tgc tgc ctc aac ccg ctg ctc tat gcc ttt      960
91 Gly Leu Gly Tyr Met His Cys Cys Leu Asn Pro Leu Leu Tyr Ala Phe
92 305      310      315      320
93 gta ggg gtc aag ttc cgg gag cgg atg tgg atg ctg ctc ttg cgc ctg      1008
94 Val Gly Val Lys Phe Arg Glu Arg Met Trp Met Leu Leu Leu Arg Leu
95      325      330      335
96 ggc tgc ccc aac cag aga ggg ctc cag agg cag cca tcg tct tcc cgc      1056
97 Gly Cys Pro Asn Gln Arg Gly Leu Gln Arg Gln Pro Ser Ser Ser Arg
98      340      345      350
99 cgg gat tca tcc tgg tct gag acc tca gag gcc tcc tac tcg ggc ttg      1104
100 Arg Asp Ser Ser Trp Ser Glu Thr Ser Glu Ala Ser Tyr Ser Gly Leu
101      355      360      365
103 <210> SEQ ID NO: 2

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104 &lt;211&gt; LENGTH: 368

105 &lt;212&gt; TYPE: PRT

106 &lt;213&gt; ORGANISM: Homo sapiens

108 &lt;400&gt; SEQUENCE: 2

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109 Met Val Leu Glu Val Ser Asp His Gln Val Leu Asn Asp Ala Glu Val
110 1          5          10          15
111 Ala Ala Leu Leu Glu Asn Phe Ser Ser Ser Tyr Asp Tyr Gly Glu Asn
112          20          25          30
113 Glu Ser Asp Ser Cys Cys Thr Ser Pro Pro Cys Pro Gln Asp Phe Ser
114          35          40          45
115 Leu Asn Phe Asp Arg Ala Phe Leu Pro Ala Leu Tyr Ser Leu Leu Phe
116          50          55          60
117 Leu Leu Gly Leu Leu Gly Asn Gly Ala Val Ala Ala Val Leu Leu Ser
118 65          70          75          80
119 Arg Arg Thr Ala Leu Ser Ser Thr Asp Thr Phe Leu Leu His Leu Ala
120          85          90          95
121 Val Ala Asp Thr Leu Leu Val Leu Thr Leu Pro Leu Trp Ala Val Asp
122          100         105         110
123 Ala Ala Val Gln Trp Val Phe Gly Ser Gly Leu Cys Lys Val Ala Gly
124          115         120         125
125 Ala Leu Phe Asn Ile Asn Phe Tyr Ala Gly Ala Leu Leu Leu Ala Cys
126          130         135         140
127 Ile Ser Phe Asp Arg Tyr Leu Asn Ile Val His Ala Thr Gln Leu Tyr
128 145         150         155         160
129 Arg Arg Gly Pro Pro Ala Arg Val Thr Leu Thr Cys Leu Ala Val Trp
130          165         170         175
131 Gly Leu Cys Leu Leu Phe Ala Leu Pro Asp Phe Ile Phe Leu Ser Ala
132          180         185         190
133 His His Asp Glu Arg Leu Asn Ala Thr His Cys Gln Tyr Asn Phe Pro
134          195         200         205
135 Gln Val Gly Arg Thr Ala Leu Arg Val Leu Gln Leu Val Ala Gly Phe
136          210         215         220
137 Leu Leu Pro Leu Leu Val Met Ala Tyr Cys Tyr Ala His Ile Leu Ala
138 225         230         235         240
139 Val Leu Leu Val Ser Arg Gly Gln Arg Arg Leu Arg Ala Met Arg Leu
140          245         250         255
141 Val Val Val Val Val Val Ala Phe Ala Leu Cys Trp Thr Pro Tyr His
142          260         265         270
143 Leu Val Val Leu Val Asp Ile Leu Met Asp Leu Gly Ala Leu Ala Arg
144          275         280         285
145 Asn Cys Gly Arg Glu Ser Arg Val Asp Val Ala Lys Ser Val Thr Ser
146          290         295         300
147 Gly Leu Gly Tyr Met His Cys Cys Leu Asn Pro Leu Leu Tyr Ala Phe
148 305         310         315         320
149 Val Gly Val Lys Phe Arg Glu Arg Met Trp Met Leu Leu Leu Arg Leu
150          325         330         335
151 Gly Cys Pro Asn Gln Arg Gly Leu Gln Arg Gln Pro Ser Ser Ser Arg
152          340         345         350
153 Arg Asp Ser Ser Trp Ser Glu Thr Ser Glu Ala Ser Tyr Ser Gly Leu

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Input Set : A:\SEQUENCE LISTING (231060.ST25).txt

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154          355          360          365
156 <210> SEQ ID NO: 3
157 <211> LENGTH: 294
158 <212> TYPE: DNA
159 <213> ORGANISM: Homo sapiens
161 <220> FEATURE:
162 <221> NAME/KEY: CDS
163 <222> LOCATION: (1)..(294)
164 <223> OTHER INFORMATION:
166 <220> FEATURE:
167 <221> NAME/KEY: mat_peptide
168 <222> LOCATION: (64)..()
169 <223> OTHER INFORMATION:
W--> 171 <400> 3
172 atg aat caa act gcg att ctg att tgc tgc ctt atc ttt ctg act cta      48
173 Met Asn Gln Thr Ala Ile Leu Ile Cys Cys Leu Ile Phe Leu Thr Leu
174   -20          -15          -10
175 agt ggc att caa gga gta cct ctc tct aga acc gta cgc tgt acc tgc      96
176 Ser Gly Ile Gln Gly Val Pro Leu Ser Arg Thr Val Arg Cys Thr Cys
177  -5          -1 1          5          10
178 atc agc att agt aat caa cct gtt aat cca agg tct tta gaa aaa ctt      144
179 Ile Ser Ile Ser Asn Gln Pro Val Asn Pro Arg Ser Leu Glu Lys Leu
180          15          20          25
181 gaa att att cct gca agc caa ttt tgt cca cgt gtt gag atc att gct      192
182 Glu Ile Ile Pro Ala Ser Gln Phe Cys Pro Arg Val Glu Ile Ile Ala
183          30          35          40
184 aca atg aaa aag aag ggt gag aag aga tgt ctg aat cca gaa tcg aag      240
185 Thr Met Lys Lys Lys Gly Glu Lys Arg Cys Leu Asn Pro Glu Ser Lys
186   45          50          55
187 gcc atc aag aat tta ctg aaa gca gtt agc aag gaa atg tct aaa aga      288
188 Ala Ile Lys Asn Leu Leu Lys Ala Val Ser Lys Glu Met Ser Lys Arg
189 60          65          70          75
190 tct cct      294
191 Ser Pro
194 <210> SEQ ID NO: 4
195 <211> LENGTH: 98
196 <212> TYPE: PRT
197 <213> ORGANISM: Homo sapiens
199 <400> SEQUENCE: 4
200 Met Asn Gln Thr Ala Ile Leu Ile Cys Cys Leu Ile Phe Leu Thr Leu
201   -20          -15          -10
202 Ser Gly Ile Gln Gly Val Pro Leu Ser Arg Thr Val Arg Cys Thr Cys
203  -5          -1 1          5          10
204 Ile Ser Ile Ser Asn Gln Pro Val Asn Pro Arg Ser Leu Glu Lys Leu
205          15          20          25
206 Glu Ile Ile Pro Ala Ser Gln Phe Cys Pro Arg Val Glu Ile Ile Ala
207          30          35          40
208 Thr Met Lys Lys Lys Gly Glu Lys Arg Cys Leu Asn Pro Glu Ser Lys
209   45          50          55

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210 Ala Ile Lys Asn Leu Leu Lys Ala Val Ser Lys Glu Met Ser Lys Arg
211 60                      65                      70                      75
212 Ser Pro
215 <210> SEQ ID NO: 5
216 <211> LENGTH: 375
217 <212> TYPE: DNA
218 <213> ORGANISM: Homo sapiens
220 <220> FEATURE:
221 <221> NAME/KEY: CDS
222 <222> LOCATION: (1)..(375)
223 <223> OTHER INFORMATION:
225 <220> FEATURE:
226 <221> NAME/KEY: mat_peptide
227 <222> LOCATION: (67)..()
228 <223> OTHER INFORMATION:
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231 atg aag aaa agt ggt gtt ctt ttc ctc ttg ggc atc atc ttg ctg gtt      48
232 Met Lys Lys Ser Gly Val Leu Phe Leu Leu Gly Ile Ile Leu Leu Val
233      -20                      -15                      -10
234 ctg att gga gtg caa gga acc cca gta gtg aga aag ggt cgc tgt tcc      96
235 Leu Ile Gly Val Gln Gly Thr Pro Val Val Arg Lys Gly Arg Cys Ser
236      -5                      -1 1                      5                      10
237 tgc atc agc acc aac caa ggg act atc cac cta caa tcc ttg aaa gac      144
238 Cys Ile Ser Thr Asn Gln Gly Thr Ile His Leu Gln Ser Leu Lys Asp
239      15                      20                      25
240 ctt aaa caa ttt gcc cca agc cct tcc tgc gag aaa att gaa atc att      192
241 Leu Lys Gln Phe Ala Pro Ser Pro Ser Cys Glu Lys Ile Glu Ile Ile
242      30                      35                      40
243 gct aca ctg aag aat gga gtt caa aca tgt cta aac cca gat tca gca      240
244 Ala Thr Leu Lys Asn Gly Val Gln Thr Cys Leu Asn Pro Asp Ser Ala
245      45                      50                      55
246 gat gtg aag gaa ctg att aaa aag tgg gag aaa cag gtc agc caa aag      288
247 Asp Val Lys Glu Leu Ile Lys Lys Trp Glu Lys Gln Val Ser Gln Lys
248      60                      65                      70
249 aaa aag caa aag aat ggg aaa aaa cat caa aaa aag aaa gtt ctg aaa      336
250 Lys Lys Gln Lys Asn Gly Lys Lys His Gln Lys Lys Lys Val Leu Lys
251 75                      80                      85                      90
252 gtt cga aaa tct caa cgt tct cgt caa aag aag act aca      375
253 Val Arg Lys Ser Gln Arg Ser Arg Gln Lys Lys Thr Thr
254      95                      100
256 <210> SEQ ID NO: 6
257 <211> LENGTH: 125
258 <212> TYPE: PRT
259 <213> ORGANISM: Homo sapiens
261 <400> SEQUENCE: 6
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263      -20                      -15                      -10
264 Leu Ile Gly Val Gln Gly Thr Pro Val Val Arg Lys Gly Arg Cys Ser
265      -5                      -1 1                      5                      10

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## VERIFICATION SUMMARY

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Input Set : A:\SEQUENCE LISTING (231060.ST25).txt

Output Set: N:\CRF4\10132004\J510121.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application No  
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:32 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:30  
L:171 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:164  
L:171 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:169  
L:230 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:223  
L:230 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:228  
L:294 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:287  
L:294 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:292  
L:348 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:9,Line#:341  
L:348 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:9,Line#:346